Amendments to the Specification

Please amend paragraph [01] as follows:

This application is a divisional application of application serial no. 10/085,134, filed March 1, 2002, allowed, which claims priority to ~~and incorporates by reference co-pending~~ provisional application Serial No. 60/272,642 filed March 1, 2001, the ~~disclosure~~ disclosures of which ~~is~~ are expressly incorporated herein.

Please amend paragraph [18] as follows:

FIG. 5. Design of primers and probes for TaqMan PCR assay. The primer and probe sequences shown are as follows: TGGAGCATGTGGTTTAATTCGA (SEQ ID NO: 5); CCTTNTGACAACTCTAGAGATAGAGCCTTCCC (SEQ ID NO: 6); TGCATGGYTGTCGTCAGCTCGTG (SEQ ID NO: 7); TGTTGGGTTAAGTCCCGCA (SEQ ID NO: 8); TGGAGCATGCGGTTTAATTCGA (SEQ ID NO: 9); CCACNAGAACTTTCCAGAGATGGATTGGTGCC (SEQ ID NO: 10); CCTANAGAAGTTTGCAGAGATGCAGATGTGCC (SEQ ID NO: 11); CCAGNTGAACTTTGCAGAGATGCATTGGTGCC (SEQ ID NO: 12); CTACNGGAATCCTCCGGAGACGGAGGAGTGCC (SEQ ID NO: 13); CCACNGGAAGTTTTCAGAGATGAGAATGTGCC (SEQ ID NO: 14); CCTCNTGACCCCTCTAGAGATAGAGTTTTCCC (SEQ ID NO: 15); CCTTNGGACAACTGCAGAGATAGAGTCTTCCC (SEQ ID NO: 16); CCCTNTGACGACTCTAGAGATAGAGTNTTNCN (SEQ ID NO: 17); CCTTNTGACCCTTCTAGAGATAGAAGTTTCCC (SEQ ID NO: 18);

GGTGGTTGCGGATCGCAGAGATGCTTTTCCTC (SEQ ID NO: 19);

ATATNGGATATAGTTAGAGATAATTATTCCCC (SEQ ID NO: 20);

CCTTNTGACAACCCTAGAGATAGGGCTTCTC (SEQ ID NO: 21);

CCACAGAATTTGGCAGAGATGCTAAAGTGC (SEQ ID NO: 22);

CCAGCTGATCACTCTAGAGATAGAGAGTGCCT (SEQ ID NO: 23);

NGCATNGYTGTCGTCAGCTCGTG (SEQ ID NO: 24).

Please amend paragraph [22] as follows:

Primers used in the present assays are able to amplify a segment of a *S. aureus* 16S rRNA gene that comprises both a conserved region and a first divergent region if a *S. aureus* 16 rRNA gene is present in a PCR reaction. The primers are virtually universal in applicability across the eubacteria. Thus the primers amplify a segment of 16S rRNA genes of other eubacteria that also has the structure of containing both a highly conserved region and a divergent region. Thus the primers employed will amplify a segment of *S. aureus* 16S rRNA in the presence of *S. aureus* DNA template. But they will amplify virtually any other eubacterial 16S rRNA in the presence of that eubacterial DNA template. Exemplary primers are shown in FIG. 5. Other primers having similar functional properties can also be used. These can be readily determined by inspection of known sequences of 16S rRNA genes or by use of computer programs such as ClustalW from the European Bioinformatics Institute ~~http://www.ebi.ac.uk/clustalw.htm~~ http://ebi.ac.uk/clustalw.htm.

Please amend paragraph [33] as follows:

The 16S rRNA gene sequences from a variety of bacterial species were obtained from GenBank. Sequence data were obtained the program Entrez (see list below). The sequences were aligned using the program ClustalW from the European Bioinformatics Institute ~~http://www.ebi.ac.uk/clustalw.htm~~ http://ebi.ac.uk/clustalw.htm. Two regions of highly conserved sequences, separated by both an internal region of highly variable sequence as well as another adjacent internal region of highly conserved sequence, were selected as the universal primer annealing sites. The internal highly conserved and highly variable sequences were used as the annealing sites of conserved and species-specific Taqman probes, respectively (Figure 1).

Please amend Table 1, on page 11, before the section heading of paragraph 33 "Design of primers and probes."

Table 1. Oligonucleotide sequences of primers and probes used in the study.

Oligonucleotides	Sequences (5' → 3')[a]	Position[b] (bp)	Fluorophores	T_m[c](°C)
Forward Primer (P890F)	TGGAGCATGTGGTTTAATTCGA (SEQ ID NO: 1)	890-912	-	59.1
Reverse Primer (P1033R)	TGCGGGACTTAACCCAACA (SEQ ID NO: 2)	1033-1051	-	58.6
Universal Probe (UniProbe)	CACGAGCTGACGACARCCATGCA (SEQ ID NO: 3)	1002-1024	VIC, TAMRA	67.3/69.3
Staph Aureus Probe (SAProbe)	CCTTTGACAACTCTAGAGATAGAGCCTTCC C (SEQ ID NO: 4)	945-978	FAM, TAMRA	65.3

[a] Sequences used for alignment *Staphylococcus aureus* (AF015929), *Staphylococcus hominis* (AY030318), *Enterococcus faecalis* (AJ276460), *Staphylococcus epidermidis* (L37605), *Enterococcus faecalis* (AJ276460), *Streptococcus pneumoniae* (X58312), *Mycoplasma pneumoniae* (AF132741), *Escherichia coli* (AF233451), *Hemophilus influenzae*, (AF224306), *Listeria pneumoniae* (M59157), *Neisseria meningitides* (AF059671), *Rickettsia rickettsii* (U11021), *Borrelia burgdorferi* (AF091368), *Bacillus anthracis* (AF290552), *Yersinia pestis* (AF366383), *Proteus mirabilis* (AF008582), and *K. pneumoniae* (AF228919)

[b] Nulceotide position based on *Staphylococcus aureus* sequences (AF015929)

[c] T_m, melting temperature.